

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

APPLICATION NO.: 09/831,088

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: INDIA L. EVANS

FOR: PLANT AMINOACYL-tRNA SYNTHETASES



CASE NO.: BB1270

GROUP ART UNIT: UNKNOWN

**STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)**Assistant Commissioner for Patents  
Washington, DC 20231

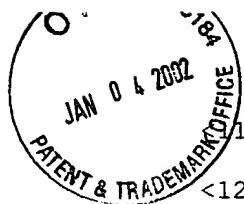
Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,

Thomas M. Rizzo, Ph.D.  
Attorney For Applicants  
Registration No. 41,272  
Telephone: 302-892-7760  
Facsimile: 302-892-1026Dated: November 15, 2001



# SEQUENCE LISTING

<10> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

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<140> US/09/831,683

<141> 2001-05-10

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 <212> PRT  
 <213> Zea mays

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 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser  
 35 40 45  
 Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser  
 50 55 60  
 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val  
 65 70 75 80  
 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu  
 85 90 95  
 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu  
 100 105 110  
 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu  
 115 120 125  
 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr  
 130 135 140  
 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu  
 145 150 155 160  
 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly  
 165 170 175  
 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp  
 180 185 190  
 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val  
 195 200 205  
 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His  
 210 215 220  
 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly  
 225 230 235 240  
 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn  
 245 250 255

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Tyr	Asp	Ala	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Lys	Leu	Met	Glu	
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	290					295					300					
Pro	Lys	Glu	Gln	Met	Arg	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser	Arg	
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Cys	Arg	Asn	Asn	Thr	Val	Glu	Glu	Asn	Leu	Ser	Leu	Trp	Lys	Glu	Met	
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Val	Asn	Gly	Thr	Glu	Arg	Gly	Met	Gln	Cys	Cys	Val	Arg	Gly	Lys	Leu	
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Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	Arg	
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Cys	Asn	Thr	Asp	Pro	His	His	Arg	Val	Gly	Ser	Lys	Tyr	Lys	Val	Tyr	
	370					375					380					
Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val	Asp	Ala	Leu	Glu	Gly	Val	
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Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln	Tyr	
				405					410					415		
Tyr	Arg	Ile	Leu	Gln	Asp	Met	Gly	Leu	Arg	Arg	Val	Glu	Ile	Tyr	Glu	
			420					425					430			
Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Leu	Leu	Ser	Lys	Arg	Lys	Leu	
		435					440					445				
Leu	Trp	Phe	Val	Gln	Asn	Lys	Lys	Val	Glu	Asp	Trp	Thr	Asp	Pro	Arg	
	450					455					460					
Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Val	Glu	Ala	
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Leu	Ile	Gln	Phe	Ile	Leu	Gln	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn	Leu	
				485					490					495		
Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Ile	Asp	Pro	
			500					505					510			
Val	Cys	Ala	Arg	His	Thr	Ala	Val	Leu	Lys	Asp	Gln	Arg	Val	Ile	Phe	
		515					520					525				
Thr	Leu	Thr	Asn	Gly	Pro	Glu	Glu	Pro	Phe	Val	Arg	Ile	Leu	Pro	Arg	
	530					535					540					
His	Lys	Lys	Phe	Glu	Gly	Ala	Gly	Lys	Lys	Ala	Thr	Thr	Phe	Ala	Asn	
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Arg	Ile	Trp	Leu	Asp	Tyr	Ala	Asp	Ala	Ala	Ala	Ile	Asn	Lys	Gly	Glu	
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Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys  
 580 585 590  
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu  
 595 600 605  
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile  
 610 615 620  
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser  
 625 630 635 640  
 Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro  
 645 650 655  
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn  
 660 665 670  
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg  
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 <213> *Oryza sativa*

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 <222> (139)  
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<220>  
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<220>  
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<210> 12

<211> 555

<212> PRT

<213> *Oryza sativa*

<220>

<221> UNSURE

<222> (130)

<223> Xaa = ANY AMINO ACID

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His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Pro Arg Arg
      20               25               30

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His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
 35               40               45

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Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
 50               55               60

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Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
 65               70               75               80

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Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
      85               90               95

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Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
 100               105               110

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Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
 115               120               125

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Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
 130               135               140

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Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys

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				165					170					175	
Glu	Ile	Gln	Gln	Glu	Leu	Glu	Lys	Gly	Thr	Pro	Tyr	Thr	Tyr	Arg	Phe
			180					185					190		
Arg	Val	Pro	Lys	Glu	Gly	Ser	Leu	Lys	Ile	Asn	Asp	Leu	Ile	Arg	Gly
		195					200					205			
Glu	Val	Ser	Trp	Asn	Leu	Asp	Thr	Leu	Gly	Asp	Phe	Val	Ile	Met	Arg
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Ser	Asn	Gly	Gln	Pro	Val	Tyr	Asn	Phe	Cys	Val	Thr	Val	Asp	Asp	Ala
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Thr	Met	Arg	Ile	Ser	His	Val	Ile	Arg	Ala	Glu	Glu	His	Leu	Pro	Asn
				245					250					255	
Thr	Leu	Arg	Gln	Ala	Leu	Ile	Tyr	Lys	Ala	Leu	Gly	Phe	Pro	Met	Pro
			260					265					270		
Ser	Phe	Ala	His	Val	Ser	Leu	Ile	Leu	Ala	Pro	Asp	Arg	Ser	Lys	Leu
	275						280					285			
Ser	Lys	Arg	His	Gly	Ala	Thr	Ser	Val	Gly	Gln	Tyr	Lys	Glu	Met	Gly
	290					295					300				
Tyr	Leu	Pro	Gln	Ala	Met	Val	Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Gly
305					310					315					320
Asp	Gly	Thr	Glu	Asn	Glu	Phe	Phe	Thr	Ile	Asp	Asp	Leu	Val	Glu	Lys
				325					330					335	
Phe	Thr	Ile	Asn	Arg	Val	Asn	Lys	Ser	Gly	Ala	Val	Phe	Asp	Ala	Val
			340					345					350		
Lys	Leu	Lys	Trp	Met	Asn	Gly	Gln	His	Leu	Arg	Ser	Phe	Pro	Pro	Asp
	355						360					365			
Val	Leu	Ile	Lys	Ser	Phe	Glu	Asp	Arg	Trp	Lys	Asp	Thr	Gly	Ile	Leu
	370					375					380				
Gln	Glu	Ser	Glu	Ser	Gly	Phe	Ala	Lys	Glu	Ala	Ala	Glu	Leu	Leu	Lys
385					390					395					400
Asp	Gly	Ile	Asp	Leu	Ile	Thr	Asp	Ala	Asp	Ala	Ala	Leu	Ser	Asn	Leu
				405					410					415	
Leu	Ser	Tyr	Pro	Leu	His	Ala	Thr	Leu	Ser	Ser	Asp	Glu	Ala	Lys	Ser
			420					425					430		
Val	Val	Gln	Asp	Lys	Leu	Ser	Glu	Val	Ala	Ser	Gly	Leu	Ile	Ser	Ala
		435					440					445			
Tyr	Asp	Ser	Gly	Glu	Leu	Cys	Gln	Ala	Leu	Ala	Glu	Gly	Arg	Asp	Gly
	450					455					460				
Trp	Gln	Lys	Trp	Val	Lys	Ile	Phe	Gly	Lys	Ser	Leu	Lys	Arg	Lys	Gly

465

470

475

480

Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His  
 485 490 495

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr  
 500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg  
 515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln  
 530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser  
 545 550 555

&lt;210&gt; 13

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Glycine max

&lt;400&gt; 13

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caaggtccaa aggtgggaaa ttgtgtctga gaattgagga cactgacttg gagaggtcca 300
caagggagtc tgaggaggcc atgctcaaag atctttcttg gcttgactt gattgggatg 360
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acaagcaatt tgcgataaac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480
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cttacactta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660
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&lt;210&gt; 14

&lt;211&gt; 404

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;400&gt; 14

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Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
 20 25 30

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr  
 35 40 45

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
 50 55 60

Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg  
 65 70 75 80

Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His  
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[illegible]



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gccctcttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcatagag 240  
gacacagatn agtcaaggac tgttcctggt gcgattgaaa aactctgcgc tgntttgaga 300  
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<210> 16  
<211> 79  
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 <223> Xaa = ANY AMINO ACID

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 Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu  
 35 40 45  
 Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu  
 50 55 60  
 Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys  
 65 70 75

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 <211> 2387  
 <212> DNA  
 <213> Zea mays

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 aattggcaat ttagtgaaga ctagggggccc cccgttgga gttttgatgg agttgagaaa 1500  
 ggagggcagc aagtttatga ataattgagg gtctgttgct gcactgaatg agctggagat 1560  
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Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
      35              40              45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
  50              55              60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
  65              70              75              80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
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Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
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Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Gly Glu Leu Cys
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Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
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Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
              165              170              175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
      180              185              190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
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Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
      210              215              220

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Cys	Gly	Val	Pro	Pro	Gln	Lys	Phe	Arg	Thr	Val	Cys	Ser	Ser	Ile	Asp	225	230	235	240
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Glu	Lys	Gly	Ile	Ser	Asn	Glu	Thr	Ala	Asp	Glu	Ile	Gly	Asn	Leu	Val	260	265	270	
Lys	Thr	Arg	Gly	Pro	Pro	Leu	Glu	Val	Leu	Met	Glu	Leu	Arg	Lys	Glu	275	280	285	
Gly	Ser	Lys	Phe	Met	Asn	Asn	Val	Gly	Ser	Val	Ala	Ala	Leu	Asn	Glu	290	295	300	
Leu	Glu	Ile	Leu	Phe	Lys	Ala	Leu	Asp	Lys	Ala	Asn	Ala	Ile	Ser	Lys	305	310	315	320
Ile	Thr	Phe	Asp	Leu	Ser	Leu	Ala	Arg	Gly	Leu	Asp	Tyr	Tyr	Thr	Gly	325	330	335	
Val	Ile	Tyr	Glu	Ala	Val	Phe	Lys	Gly	Ala	Ala	Gln	Val	Gly	Ser	Ile	340	345	350	
Ala	Ala	Gly	Gly	Arg	Tyr	Asp	Asn	Leu	Val	Gly	Met	Phe	Ser	Gly	Lys	355	360	365	
Gln	Ile	Pro	Ala	Val	Gly	Val	Ser	Leu	Gly	Ile	Glu	Arg	Val	Phe	Ala	370	375	380	
Ile	Met	Glu	Gln	Gln	Glu	Lys	Glu	Arg	Asn	Glu	Lys	Ile	Arg	Pro	Thr	385	390	395	400
Glu	Thr	Glu	Val	Leu	Val	Ser	Ile	Leu	Gly	Lys	Asp	Leu	Thr	Leu	Ala	405	410	415	
Ala	Glu	Leu	Val	Ser	Glu	Leu	Trp	Asn	Ala	Gly	Ile	Lys	Ala	Glu	Phe	420	425	430	
Lys	Leu	Thr	Thr	Arg	Val	Ala	Asn	His	Ile	Lys	Tyr	Ala	Leu	Gln	Ser	435	440	445	
Ser	Ile	Pro	Trp	Met	Val	Leu	Val	Gly	Glu	Ser	Glu	Leu	Gln	Lys	Gly	450	455	460	
Thr	Val	Lys	Leu	Lys	Asp	Val	Glu	Ala	Asn	Gln	Glu	Glu	Glu	Val	Asp	465	470	475	480
Arg	Lys	Asp	Phe	Val	Arg	Glu	Leu	Lys	Lys	Arg	Leu	Ser	Lys	Ser		485	490	495	

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gtcgaaaggt	tctgcaagaa	gtattaaatt	gttattcagt	accagaaaat	ttatttggca	180
aggtctgcgt	cattattgat	aaaattgaga	aaattccagc	tgacgagata	aagaaagagt	240
tgaaagctgt	tggtctatct	caagaggctg	tccaggagct	attgcaagtc	ctttctgtga	300
agtcattgac	cgagttagaa	gagagacttg	ggagcagtg	ggaagcagtt	gctgatctga	360
aacagctatt	ctcccttgct	gaaaaaattg	gttactctaa	atggcttcaa	tttgatgcat	420
cagttgttcg	aggtcttgct	tactacactg	gcattgtatt	tgagggtttt	gaccgagaag	480
gaaagctgcg	agctatctgt	ggtggtggtc	gatatgatca	tttgttctca	acttttggtg	540
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aaaagagaan	ggtctgttac	cgggaagctt	aacttgcaaa	tagatgacat	tgtgtgtgcc	660
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20 25 30  
Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
35 40 45  
Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
50 55 60  
Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
65 70 75 80  
Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val  
85 90 95  
Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser  
100 105 110  
Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys  
115 120 125  
Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly  
130 135 140  
Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly  
145 150 155 160  
Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser  
165 170 175  
Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp  
180 185 190  
Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu  
195 200 205  
Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys  
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Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile  
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<212> DNA

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tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180

gtcatctgaa	gcagtacagg	gcattcattga	agtgtctctct	ctcaagtcac	tgtccaaact	240
tgaagaggtg	ctaggctcag	gtgttgaagc	cgttgctgac	ttgaagaagc	tcttctcgct	300
tgctgagcaa	tatggttatt	ctgattggat	ctgtttcgat	gcattctgtt	ttcgtggcct	360
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 Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg  
 35 40 45  
 Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala  
 50 55 60  
 Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu  
 65 70 75 80  
 Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys  
 85 90 95  
 Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe  
 100 105 110  
 Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe  
 115 120 125  
 Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly  
 130 135 140  
 Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala  
 145 150 155 160  
 Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu  
 165 170 175  
 Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe  
 180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys  
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu  
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile  
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile  
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 tcaatgttga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240  
 ttgacatggg ttccagtgcg gcaaagatgg ccggttggct cccagatcca agtgaagaaga 300  
 agtttccgaa aacaagccat gttggatttg gtcttgttct tgggttcaaga tggcaagcgg 360  
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 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480  
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 His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr  
 35 40 45  
 Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln  
 50 55 60  
 Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
 65 70 75 80  
 Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa

Glu	Lys	Lys	Phe	Pro	Lys	Thr	Ser	His	Val	Gly	Phe	Gly	Leu	Phe	Leu
			100					105					110		
Val	Gln	Asp	Gly	Lys	Arg	Phe	Arg	Thr	Arg	Ser	Thr	Glu	Val	Val	Arg
		115					120					125			
Leu	Val	Glu	Leu	Leu	Asp	Glu	Ala	Lys	Ser	Arg	Ser	Lys	Ser	Glu	Leu
		130				135						140			
Thr	Glu	Asn	Gly	Lys	Ile	Val	Asp	Trp	Thr	Asp	Xaa	Glu	Leu	Glu	Gln
145					150					155					160
Thr	Ser	Glu	Ala	Val	Gly	Tyr	Gly	Ala	Val	Lys	Tyr	Ala	Asp	Leu	Lys
				165					170					175	
Asn	Asn	Arg	Leu	Thr	Asn	Tyr	Thr	Phe	Ser	Phe	Glu	Gln	Met	Leu	Ser
			180					185					190		
Asp	Lys	Gly	Asn	Thr	Ala	Val	Tyr	Leu	Gln	Tyr	Ala	His	Ala	Arg	Ile
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ggttttggg attaccagt caacaatgct atgagtgtat tttcaagaat aagaggatcc 180  
gcaacaaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240  
tcaaataatta tcgaatccat ctctgttgcc ggancgtggt acattaacat aacgttatcc 300  
agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360  
gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420  
aaaaagaana tgcaagtgg gcaataatna agncaacaa taaatngggg natancccaa 480  
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20 25 30  
Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val  
35 40 45  
Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala  
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Gln Arg Ile Gln  
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<220>  
<221> unsure  
<222> (286)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (288)  
<223> n = A, C, G or T

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<222> (325)  
<223> n = A, C, G or T

<220>  
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<222> (342)  
<223> n = A, C, G or T

<220>  
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<222> (373)  
<223> n = A, C, G or T

<400> 27  
gttgagggtg tagacatncc acttattgct gtganaagag atgggtggcta naactatitt 60  
acaactgata tagcatcact ttggtatcgt cttaatgaag aaaaacttga atggattgta 120  
tatgttacag atattgggca gcaacagcac ttgatatnc tattnaaggc ctataggcgt 180  
gcagggttggg taccaaagga tgagaatgcg tatccaaaat gtactcatat aggttttggg 240  
cttgttcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tggtcgatta 300  
gttgattact tgatgaagct aaaangcgct gtaaaattgc cntcttgaaa cgtgatacaa 360  
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28  
<211> 115

<212> PRT  
 <213> Glycine max  
 <220>  
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 <222> (6)  
 <223> Xaa = ANY AMINO ACID

<220>  
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 <222> (12)  
 <223> Xaa = ANY AMINO ACID

<220>  
 <221> UNSURE  
 <222> (17)  
 <223> Xaa = ANY AMINO ACID

<220>  
 <221> UNSURE  
 <222> (53)  
 <223> Xaa = ANY AMINO ACID

<220>  
 <221> UNSURE  
 <222> (55)  
 <223> Xaa = ANY AMINO ACID

<220>  
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 <222> (94)  
 <223> Xaa = ANY AMINO ACID

<220>  
 <221> UNSURE  
 <222> (96)  
 <223> Xaa = ANY AMINO ACID

<220>  
 <221> UNSURE  
 <222> (109)  
 <223> Xaa = ANY AMINO ACID

<400> 28  
 Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly  
 1 5 10 15  
 Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn  
 20 25 30  
 Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
 35 40 45  
 Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
 50 55 60  
 Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
 65 70 75 80  
 Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa

Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys  
 100 105 110

Leu Pro Ser  
 115

<210> 29  
 <211> 565  
 <212> DNA  
 <213> Triticum sp.

<220>  
 <221> unsure  
 <222> (350)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (378)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (408)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (414)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (432)  
 <223> n = A, C, G or T

<220>  
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 <222> (433)  
 <223> n = A, C, G or T

<220>  
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 <222> (444)  
 <223> n = A, C, G or T

<220>  
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 <222> (452)  
 <223> n = A, C, G or T

<220>  
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 <222> (458)  
 <223> n = A, C, G or T

<220>  
 <221> unsure

<222> (466)  
<223> n = A, C, G or T

<220>  
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<222> (487)  
<223> n = A, C, G or T

<220>  
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<222> (494)  
<223> n = A, C, G or T

<220>  
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<222> (503)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (523)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (535)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (539)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (548)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (555)  
<223> n = A, C, G or T

<400> 29  
tgtttttcaa ggctgccagg atggctgggtt ggctttccaga tccaaaggaa aagaagttcc 60  
caaaaacgag tcatgttggg tttggccttg ttcttggagc agatggcaag cgcttccgaa 120  
ctcgtagtac tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180  
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattggtga ctggactgat 240  
gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300  
tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360  
agggaataac tgctgtcnac ttcaataagc caagcccgtg cctcccanca ttcnaaaacc 420  
caacatggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480  
gggacgnact aacngtatgc aanatggtta aaggatgaca acncttccaa tgtcngggng 540  
aaactatnac taccnaagta aaagt 565

<210> 30  
<211> 33  
<212> PRT  
<213> Triticum sp.



<400> 30  
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
 1 5 10 15

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 20 25 30

Leu

<210> 31  
 <211> 546  
 <212> DNA  
 <213> Oryza sp.

<220>  
 <221> unsure  
 <222> (448)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (512)  
 <223> n = A, C, G or T

<400> 31  
 atcactatatt cccctgatg tactcatcaa gagttttgag gatagatgga aggacacagg 60  
 cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg 120  
 catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgtcgt atccccctcca 180  
 tgctacatta agcagtgatg aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc 240  
 atcaggactc atttctgctt atgatagcgg tgaactttgt caagcactag ctgagggccg 300  
 tgatggtttg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360  
 actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420  
 caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcaactcaaca atccggtttc 480  
 gtaaattctcg acgagaggtc agaattcctga angagtggag tggagtcact ggtacaggac 540  
 aagatc 546

<210> 32  
 <211> 147  
 <212> PRT  
 <213> Oryza sp.

<400> 32  
 Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr  
 1 5 10 15

Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu  
 20 25 30

Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu  
 35 40 45

Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu  
 50 55 60

Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu  
 65 70 75 80

Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly  
 85 90 95

Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys  
100 105 110

Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly  
115 120 125

Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys  
130 135 140

Ala Gly Thr  
145

<210> 33  
<211> 524  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (386)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (423)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (459)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (481)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (483)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (486)  
<223> n = A, C, G or T

<400> 33  
aaatggcgct gttgtgtggc ggcatgccat ggtcgaaggt gatagttcct cccattttcc 60  
accactctca caccctctgc accttcttct tccaacgacg ccgtttctca gtctctgctc 120  
tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180  
acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaaggtcc aaaggtggga 240  
aatttgtgct gagaattgag gacactgact tggagagggt caagtaggga gtctgaggag 300  
gccatgctca aagatctttc ttggcttgga cttgattggg atgaagggcc tgggtgttgg 360  
aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420  
ggngaaacta cacaaatccg ggcaagtta accgctgcnt tctgggtccaa agagggaact 480  
nanagnaaat gaaaggagggt tgctaaacta aagcaactgg cccc 524

<210> 34

<211> 94  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (63)  
<223> Xaa = ANY AMINO ACID

<400> 34  
Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro  
1 5 10 15  
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
20 25 30  
Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
35 40 45  
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser  
50 55 60  
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
65 70 75 80  
Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro  
85 90

<210> 35  
<211> 506  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (18)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (483)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (505)  
<223> n = A, C, G or T

<220>  
<221> unsure  
<222> (506)  
<223> n = A, C, G or T

<400> 35  
ggaacatgga tattattngt gttcccgggg ttatggctga agcagagctt atagcttcta 60  
tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aaggtttcca 120  
gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttgga 180  
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
tgaaagctgt tggctctatc caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
agtcattgac cgagttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360

acagtattct cccttgctga aaaaattggt tactctaaat ggttcaattt gatgatagtt 420  
 gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480  
 gcntctgtgt gtgtcaatac attgnn 506

<210> 36  
 <211> 48  
 <212> PRT  
 <213> Glycine max

<400> 36  
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
 1 5 10 15  
 Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 20 25 30  
 Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 35 40 45

<210> 37  
 <211> 577  
 <212> DNA  
 <213> Triticum sp.

<220>  
 <221> unsure  
 <222> (140)  
 <223> n = A, C, G or T

<220>  
 <221> unsure  
 <222> (370)  
 <223> n = A, C, G or T

<220>  
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 <222> (411)  
 <223> n = A, C, G or T

<220>  
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 <222> (413)  
 <223> n = A, C, G or T

<220>  
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 <222> (469)  
 <223> n = A, C, G or T

<220>  
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 <222> (481)  
 <223> n = A, C, G or T

<220>  
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 <222> (504)  
 <223> n = A, C, G or T

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<220>  
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 <222> (530)  
 <223> n = A, C, G or T

<220>  
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<220>  
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 <222> (556)  
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<220>  
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 <222> (564)  
 <223> n = A, C, G or T

<400> 37  
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 gtgtttggata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120  
 aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180  
 tctgaagcag tacagggcat cattgaagtg ctctctctca agtcactgtc caaacttgaa 240  
 gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaacctctt ctgcttgc 300  
 gagcaatatg gttattctga ttggatctgt ttgatgcat ctgttggtcg tggccttgca 360  
 tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420  
 ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccaccctgtg 480  
 nctttggatt tggaatcctg tcanagtga ctcnaaaga aaggtcttn ctacctgcac 540  
 tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38  
 <211> 46  
 <212> PRT  
 <213> Triticum sp.

<220>  
 <221> UNSURE  
 <222> (38)  
 <223> Xaa = ANY AMINO ACID

<400> 38  
 Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr  
 1 5 10 15  
 Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys  
 20 25 30  
 Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile  
 35 40 45